

IN THE CLAIMS

Claims 1, 36, and 42 have been amended. Claims 27, 46, 50-56, 69-70, 75, and 79 have been cancelled. New claims 80-93 have been added. Claims 1, 11, 34, 36, 42, 43, and 80-93 are pending in the present application. The following is the status of the claims of the above-captioned application, as amended.

1. (Currently Amended) A method for determining the mode of action of an antimicrobial compound, comprising:

(a) detecting hybridization complexes formed by contacting at least one nucleic acid sample, obtained by culturing cells of a ~~bacterium~~ Bacillus subtilis in the presence of at least one sub-inhibitory amount of an antimicrobial compound having an unknown mode of action, with a plurality of nucleic acid sequences corresponding to genes of the ~~bacterial~~ Bacillus subtilis cells, wherein the presence, absence or change in the amount of the hybridization complexes detected, compared with hybridization complexes formed between the plurality of nucleic acid sequences and a second nucleic acid sample obtained from the ~~bacterial~~ Bacillus subtilis cells cultured in the absence or presence of a standard compound having a known mode of action, is indicative of the similarity or dissimilarity of the mode of actions of the antimicrobial compound and the standard compound; and

(b) assigning a mode of action for the antimicrobial compound based on the similarity or dissimilarity of values assigned to the hybridization complexes detected in (a) based on the relative amount of hybridization to a second set of hybridization values assigned to the hybridization complexes formed from the second nucleic acid sample.

2-10. (Cancelled).

11. (Original) The method of claim 1, wherein the antimicrobial compound is a member of the class of antimicrobial compounds that inhibit cell wall synthesis, interfere with the cell membrane, inhibit protein synthesis, inhibit topoisomerase activity, inhibit RNA synthesis, or is a competitive inhibitor.

12-26. (Cancelled)

27. (Original) The method of claim 1, wherein the plurality of sequences are obtained from *Bacillus subtilis*.

28-33. (Cancelled)

34. (Original) The method of claim 1, wherein the plurality of nucleic acid sequences is contained on a substrate.

35. (Cancelled)

36. (Currently Amended) The method of claim 1, further comprising:

(c) identifying from the plurality of nucleic acid sequences at least one sequence, ~~or a homolog thereof~~, from the nucleic acid sample obtained from the ~~bacterial~~ *Bacillus subtilis* cells cultivated in the presence of the antimicrobial compound that has a detected expression level that is significantly different from the nucleic acid sample obtained from ~~bacterial~~ *Bacillus subtilis* cells cultivated in the absence of the antimicrobial compound.

37-41. (Cancelled)

42. (Currently Amended) The method of claim 36, further comprising:

(d) isolating a sequence identified in (c) ~~or a homolog thereof~~.

43. (Original) The method of claim 42, wherein the sequence is a marker of the antimicrobial compound.

44-79. (Cancelled)

80. (New) The method of claim 1, wherein the step in (b) comprises subjecting the values to a program for analysis.

81. (New) The method of claim 80, wherein the program for analysis comprises a computer algorithm.
82. (New) The method of claim 1, wherein the plurality of sequences correspond to less than about 75% of the genome of the *Bacillus subtilis* cells.
83. (New) The method of claim 1, wherein the plurality of sequences correspond to less than about 50% of the genome of the *Bacillus subtilis* cells.
84. (New) The method of claim 1, wherein the plurality of sequences correspond to less than about 25% of the genome of the *Bacillus subtilis* cells.
85. (New) The method of claim 1, wherein the plurality of sequences correspond to less than about 10% of the genome of the *Bacillus subtilis* cells.
86. (New) The method of claim 1, wherein the plurality of sequences correspond to less than about 5% of the genome of the *Bacillus subtilis* cells.
87. (New) The method of claim 1, wherein the plurality of sequences correspond to less than about 2% of the genome of the *Bacillus subtilis* cells.
88. (New) The method of claim 34, wherein the substrate is a microarray, macroarray, Southern blot, zoo blot, slot blot, dot blot, or Northern blot.
89. (New) The method of claim 36, wherein the difference in the detected expression level is at least about 10% or greater.
90. (New) The method of claim 36, wherein the difference in the detected expression level is at least about 20% or greater.
91. (New) The method of claim 36, wherein the difference in the detected expression level is at least about 50% or greater.

92. (New) The method of claim 36, wherein the difference in the detected expression level is at least about 75% or greater.

93. (New) The method of claim 36, wherein the difference in the detected expression level is at least about 100% or greater.